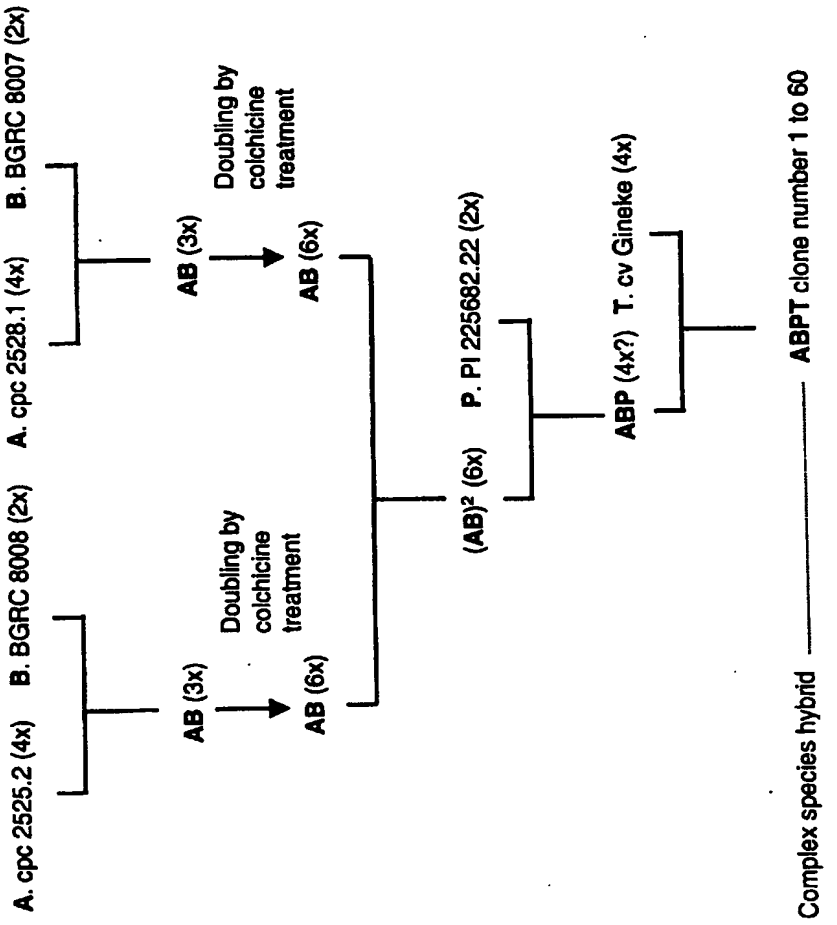

A. cpc 2525.2 (4x)
B. BGRC 8008 (2x)
AB (3x)
Doubling by colchicine treatment
AB (6x)
A. cpc 2528.1 (4x)
B. BGRC 8007 (2x)
AB (3x)
Doubling by colchicine treatment
AB (6x)
(AB)² (6x)
P. PI 225682.22 (2x)
ABP (4x?)
T. cv Gineke (4x)
Complex species hybrid
ABPT clone number 1 to 60

Figure 1A

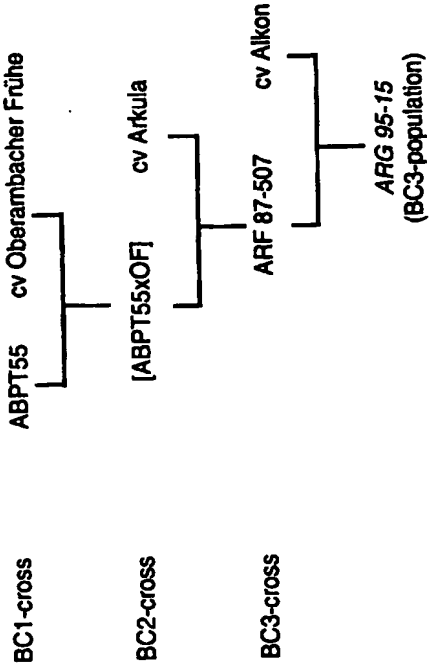

BC1-cross
ABPT55
cv Oberambacher Frühe
BC2-cross
[ABPT55xOF]
cv Arkula
BC3-cross
ARF 87-507
cv Alkon
ARG 95-15
(BC3-population)

Figure 1B

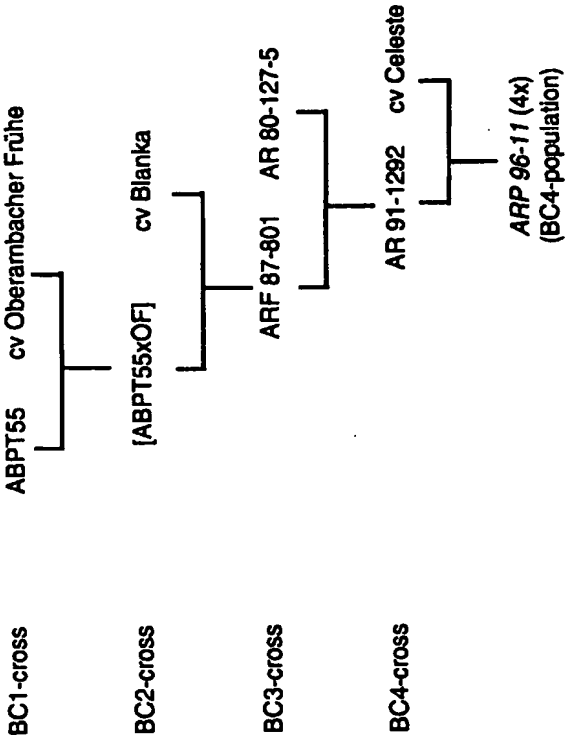

BC1-cross
ABPT55
cv Oberambacher Frühe
BC2-cross
[ABPT55xOF]
cv Blanka
BC3-cross
ARF 87-801
AR 80-127-5
BC4-cross
AR 91-1292
cv Celeste
ARP 96-11 (4x)
(BC4-population)

Figure 1C

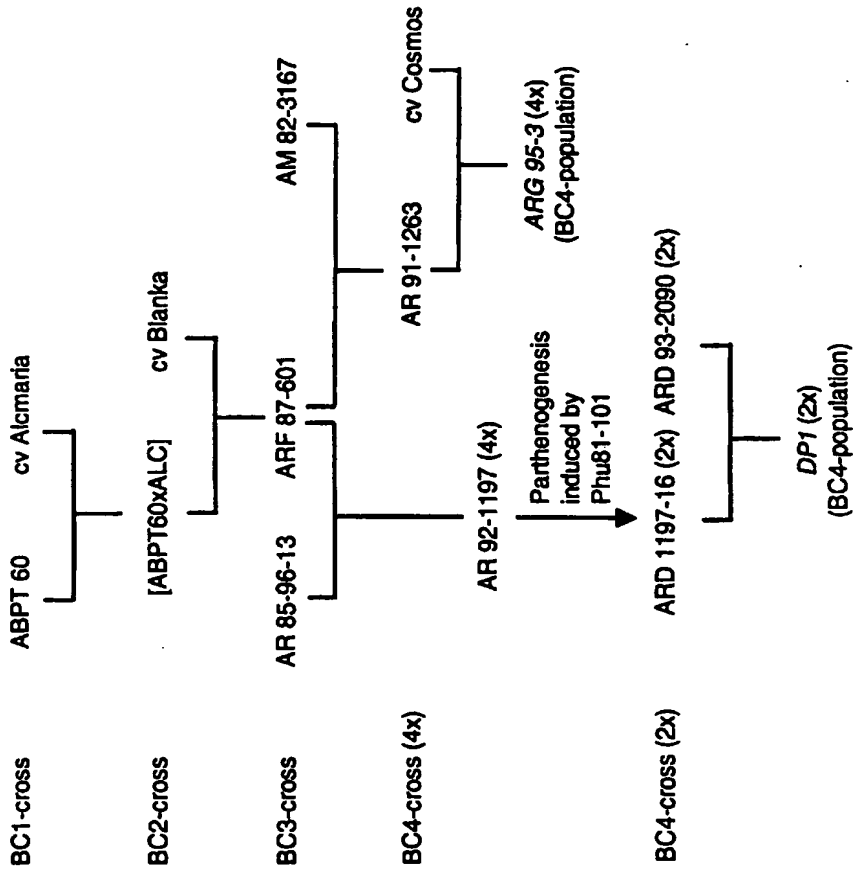

BC1-cross
ABPT 60
cv Alcmaria
BC2-cross
[ABPT60xALC]
cv Blanka
BC3-cross
AR 85-96-13
ARF 87-601
AM 82-3167
BC4-cross (4x)
AR 92-1197 (4x)
AR 91-1263
cv Cosmos
Parthenogenesis induced by Phu81-101
ARG 95-3 (4x) (BC4-population)
BC4-cross (2x)
ARD 1197-16 (2x)
ARD 93-2090 (2x)
DP1 (2x) (BC4-population)

Figure 1D

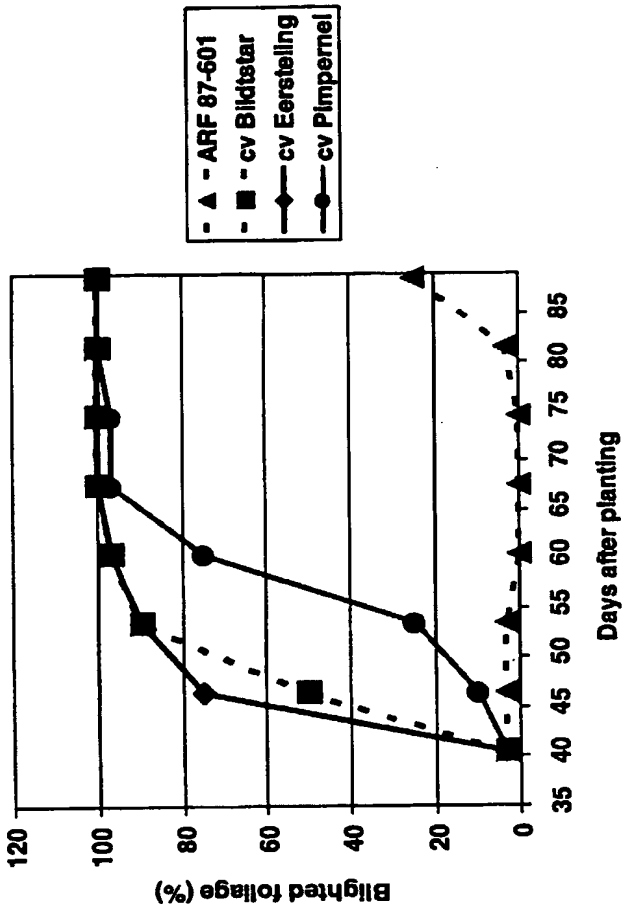

ARF 87-601
cv Bildstar
cv Eersteling
cv Pimpernel
Blighted foliage (%)
120
100
80
60
40
20
0
35
40
45
50
55
60
65
70
75
80
85
Days after planting

Figure 2

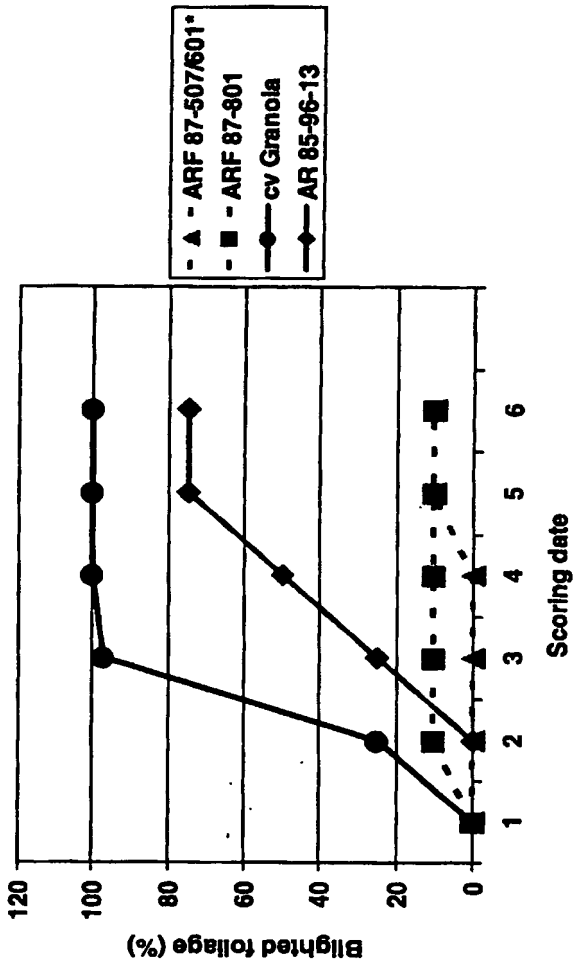


Figure 3

* ARF 87-507 and ARF 87-601 had identical disease progress curves

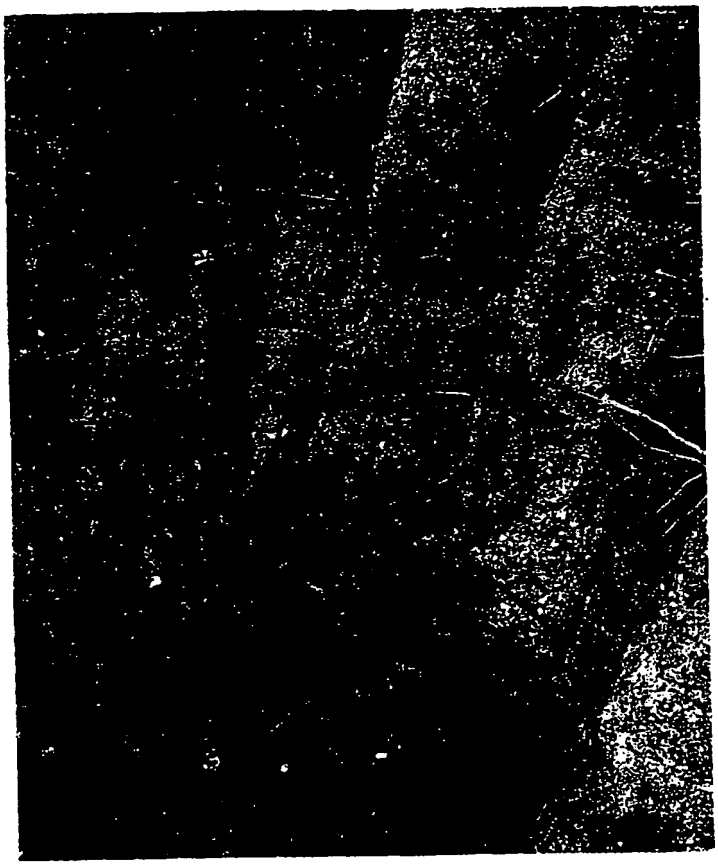


Figure 4

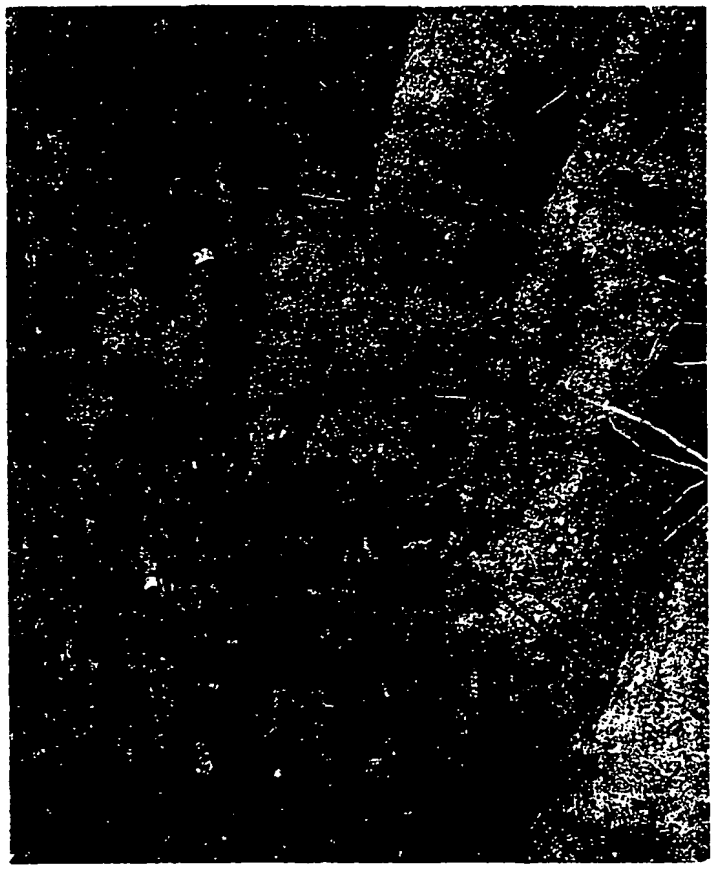
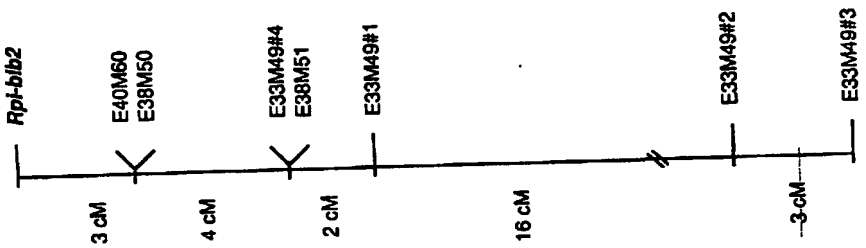


Figure 4 dia 3

Figure 4 dia 4

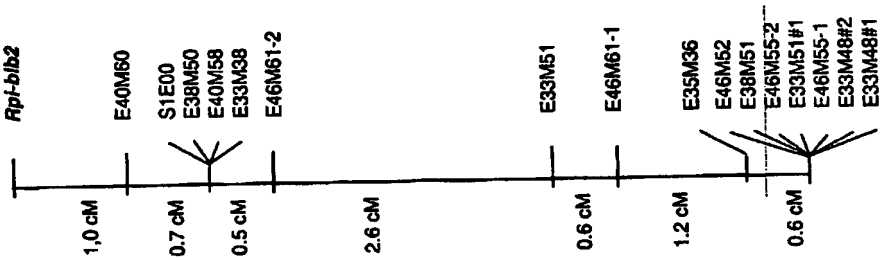
Figure 4 dia 5

Figure 4 dia 6



ARG 95-15

Figure 5



ARG 95-3

Figure 6

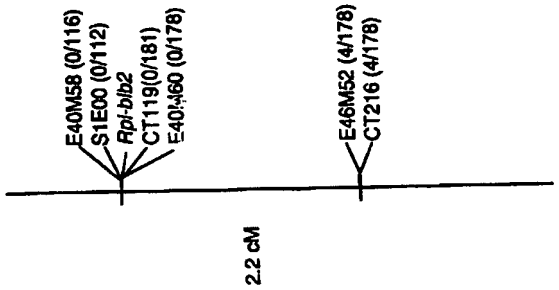

E40M58 (0/116)
S1E00 (0/112)
Rpi-blb2
CT119(0/181)
E40M60 (0/178)
E46M52 (4/178)
CT216 (4/178)
2.2 cM
ARG 95-3

Figure 7

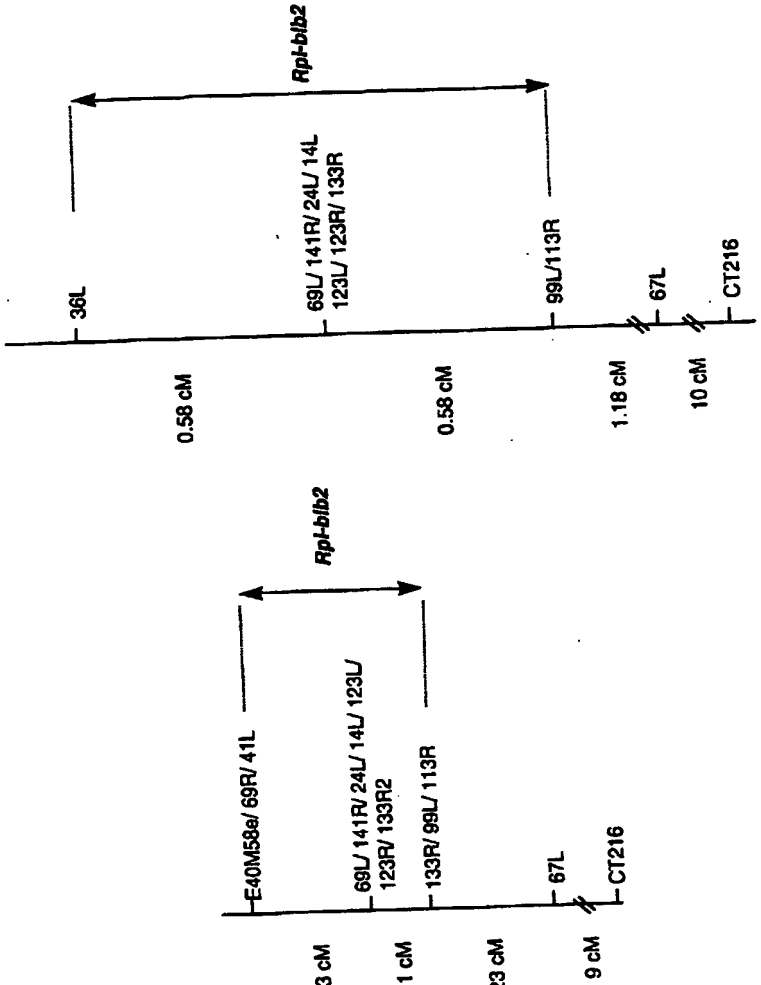

Rpi-blb2
36L
69L/ 141R/ 24L/ 14L
123L/ 123R/ 133R
99L/113R
67L
CT216
0.58 cM
0.58 cM
1.18 cM
10 cM
ARP 96-11
Rpi-blb2
E40M58a/ 69R/ 41L
69L/ 141R/ 24L/ 14L/ 123L/
123R/ 133R2
133R/ 99L/ 113R
67L
CT216
0.23 cM
0.11 cM
0.23 cM
9 cM
ARG 95-3

Figure 8

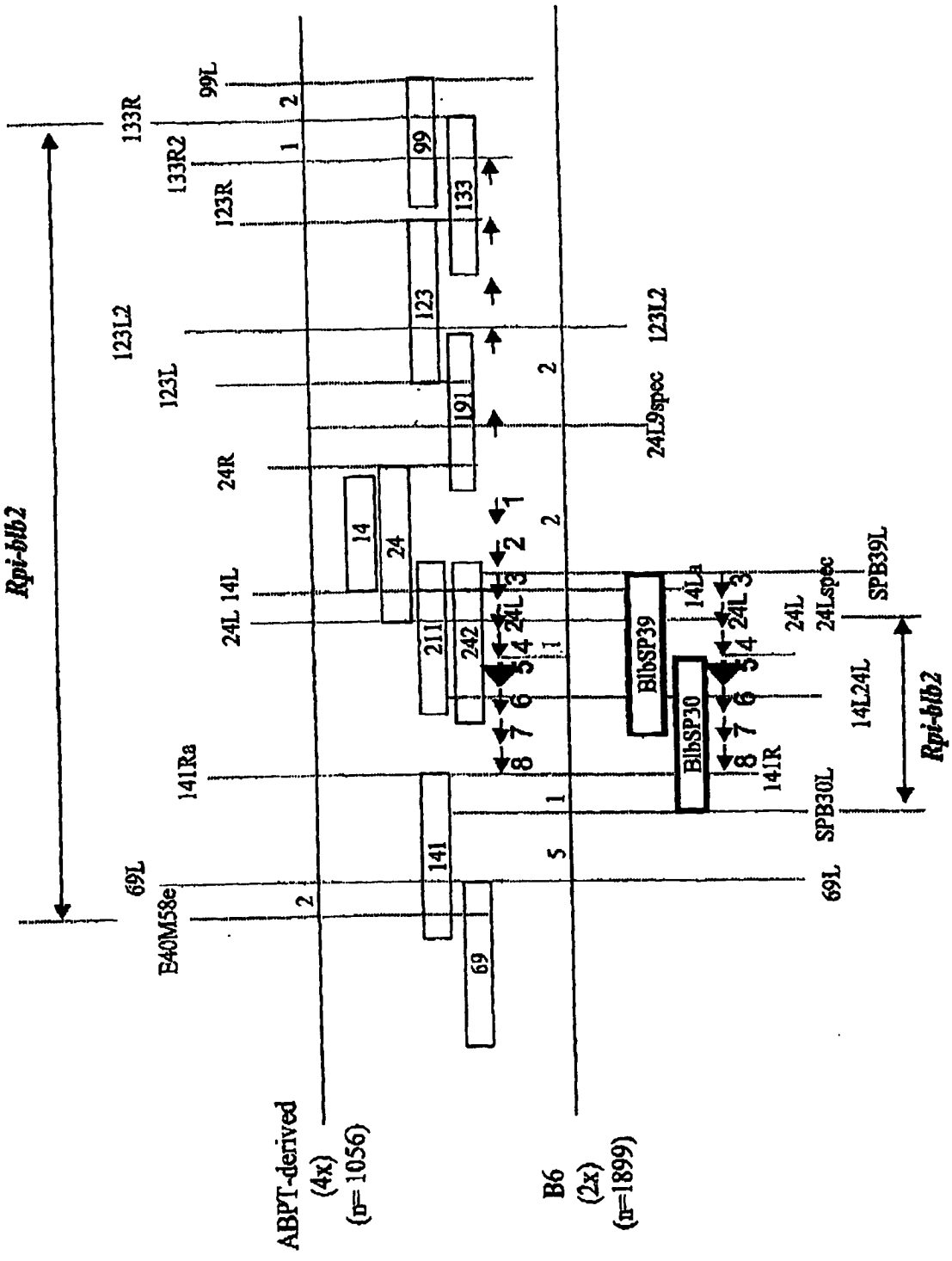

Rpi-blb2
69L
E40M58e
141Ra
24L 14L
24R
123L
123L2
133R2
133R
99L
ABPT-derived
(4x)
(n= 1056)
B6
(2x)
(n=1899)
BlbSP39
BlbSP30
141R
24L
24Lspec
SPB39L
SPB30L
14L24L
Rpi-blb2

Figure 9

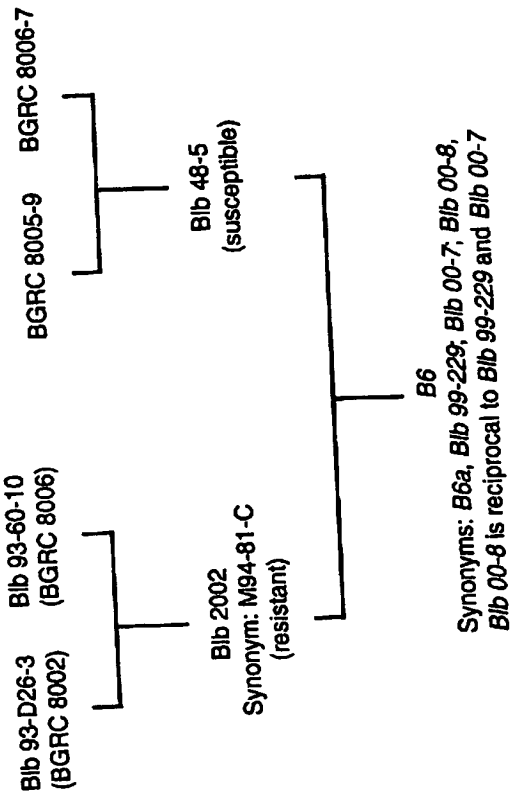

BGRC 8006-7
BGRC 8005-9
Blb 48-5
(susceptible)
Blb 93-60-10
(BGRC 8006)
Blb 93-D26-3
(BGRC 8002)
Blb 2002
Synonym: M94-81-C
(resistant)
B6
Synonyms: B6a, Blb 99-229; Blb 00-7; Blb 00-8,
Blb 00-8 is reciprocal to Blb 99-229 and Blb 00-7

Figure 10

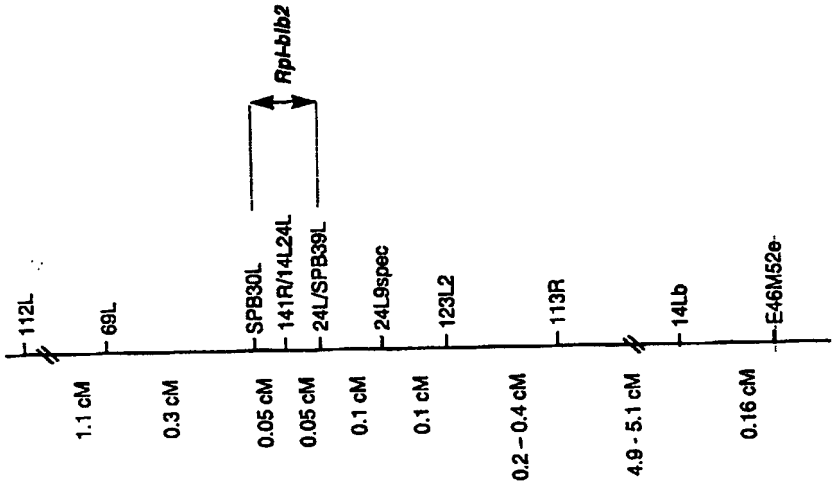

Rpi-blb2
112L
69L
SPB30L
141R/14L24L
24L/SPB39L
24L9spec
123L2
113R
14Lb
E46M52e
1.1 cM
0.3 cM
0.05 cM
0.05 cM
0.1 cM
0.1 cM
0.2 – 0.4 cM
4.9 - 5.1 cM
0.16 cM
B6

Figure 11

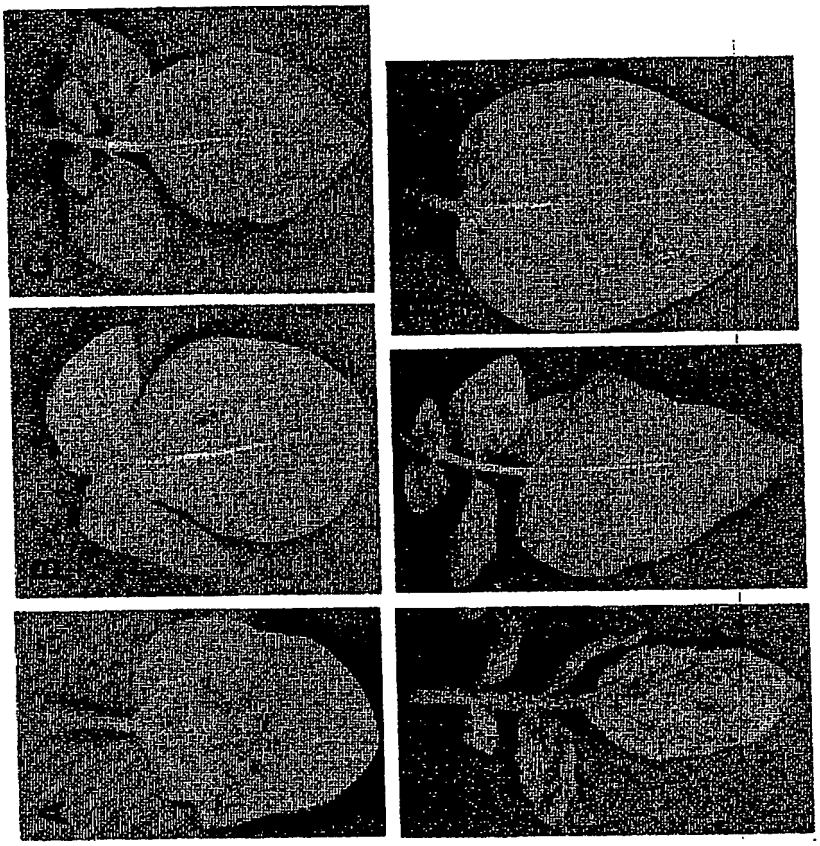


Figure 12

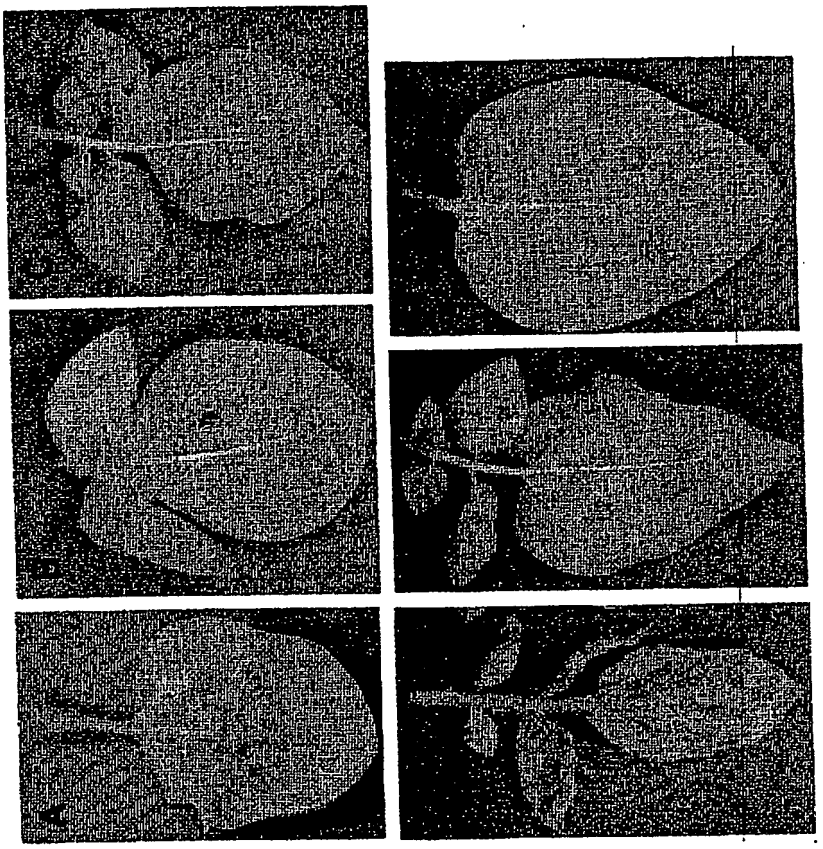


Figure 12 dia2

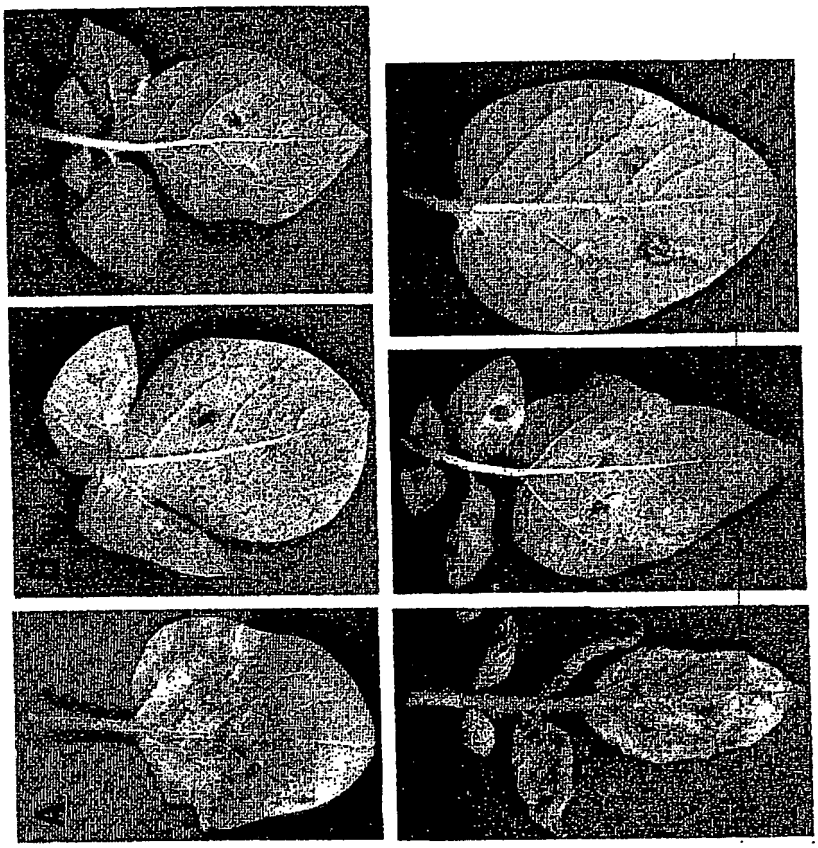


Figure 12 dia 3

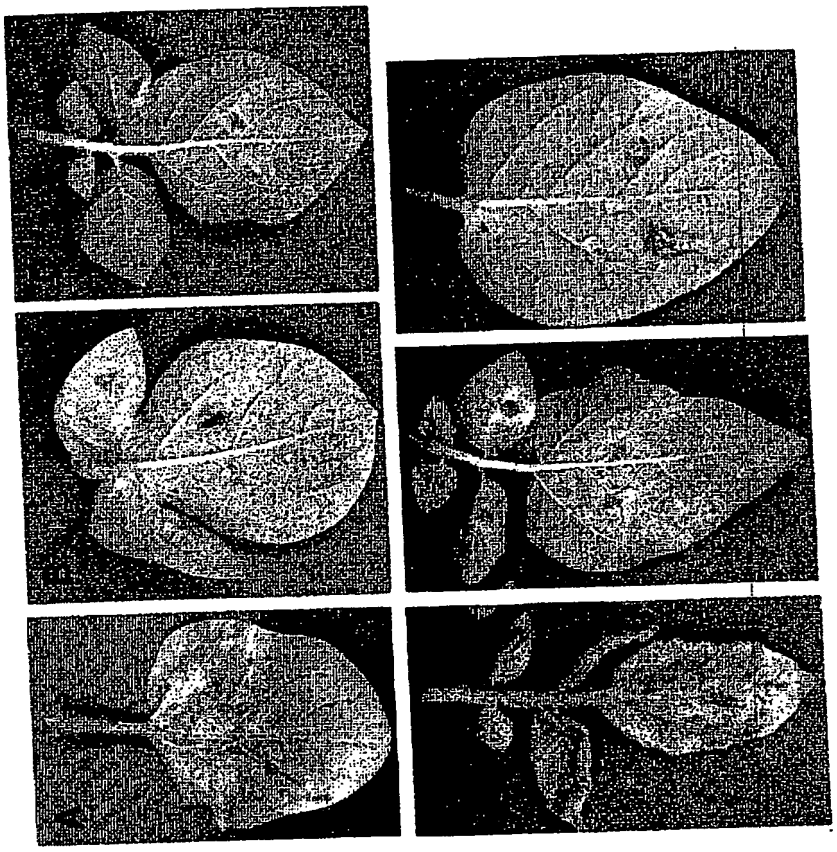


Figure 12 dia 4

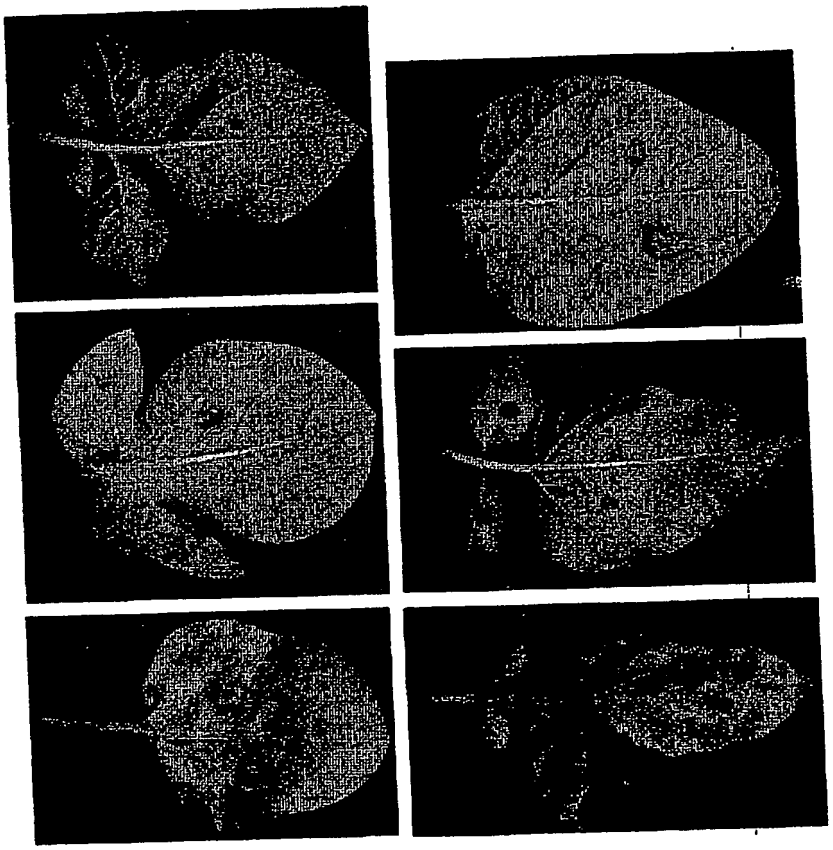


Figure 12 dia 5

Figure 13A

```
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CTGAAATTGAAGCTGACATTTATTTGTACATATGTCCAGCTTTCTTATTC 200
CGATTTGGAGAAGTTTGAAGATATAATGACTAGAAAAAGACAAGAGGTTG 250
AGAATCTGCTTCAACCAATTTTGGATGATGATGGCAAAGACGTCGGGTGT 300
AAATATGTCCTTACTAGCCTCGCCGGTAATATGGATGACTGTATAAGCTT 350
GTATCATCGTTCTAAATCAGATGCCACCATGATGGATGAGCAATTGGGCT 400
TCCTCCTCTTGAATCTCTCTCATCTATCCAAGCATCGTGCTGAAAAGATG 450
TTTCCTGGAGTGACTCAATATGAGGTTCTTCAGAATGTATGTGGCAACAT 500
AAGAGATTTCCATGGATTGATAGTGAATTGTTGCATTAAGCATGAGATGG 550
TTGAGAATGTCTTATCTCTGTTTCAACTGATGGCTGAGAGAGTAGGACGC 600
TTCCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGA 650
TGAGGATGATCAGAATGATAAAGACCCTCAACTCTTCAAGCTAGCACATC 700
TACTCTTGAAGATTGTTCCAACTGAATTGGAGGTTATGCACATATGTTAT 750
AAAACTTTGAAAGCTTCAACTTCAACAGAAATTGGACGCTTCATTAAGAA 800
GCTCCTGGAAACCTCTCCGGACATTCTCAGAGAATATCTGATTCATCTAC 850
AAGAGCATATGATAACTGTTATTACCCCTAACACTTCAGGGGCTCGAAAC 900
ATTCATGTCATGATGGAATTCCTATTGATTATTCTTTCTGATATGCCGCC 950
CAAGGACTTTATTCATCATGACAAACTTTTTGATCTCTTGGCTCGTGTTG 100
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TCTGGAAAATATTGAACTCCTTAAGGAAGATCTCAAACATGTTTATCTGA 1150
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TTATTCAATTGCTTTGATAAAGGAACAAATTGGGCTGGTGAAAGAAGACT 1300
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CAAGAAACCAGTTGAGAGCAAGTCATTGACAACTGATAAAATAATTGTAG 1600
GTTTTGGTGAGGAGACAAACTTGATACTTAGAAAGCTCACCAGTGGACCG 1650
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ATCTTATTGTCTTAGATGACGTGTGGGATACTAATACATGGGATGAGCTA 1950
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GGAGGGGACGAGCTTCAGATCCTTGGCCAGAAGGATATCCCGTTATTTAA 3800
GTAG 3804

Figure 13B

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*AAAAATTTGATATGTGTTATTTTGGCAG*GAGTCATTTTCTGCTCTTCGCA 150
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GATCAAAAGGCTGTTGATGTGGATCTGATTGAAAGCCTGAAATTGAAGCT 2501
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GGAATTCCTATTGATTATTCTTTCTGATATGCCGCCCAAGGACTTTATTC 1050
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Figure 13C

GATCTAGAATCACCGAACCTCCCCTCGGTACAGCTCCTCCAGTTCTACCA 50
TGAATTTCATCCACTGATTCCTCTTCAATCGCCATTGCAGATTCTCTCGA 100
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Figure 13D

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TGACTTTTTATGCTGCTTTTGATCTTCAGTTTCTTGTATTCTTTTTCTAC 7550
TGCTTTCCTCTTCTTTCTCCTGAGTAAAGTTTTATGTAGGTACTTTTTAT 7600
ACGTCCGATCGTGAGAACTTGAAAGAAAGCTCTCTATAGCTATGTTAGGT 7650
GCCCACATAAAAAAATGAAATATTACAAAAACCCTGATAATAAAATACAC 7700
TAATCTAAGATATTCACTGCAACATACATGCAAAATATATATATATAAAT 7750
TTTCATGAAAATTATAACAAATAATAGATGTGAACATATAACTTTAAAAA 7800
TAATATTACATCCATAAAGCTTAAATTCTAGATCCATCTATGCTTGTATG 7850
ATGCATAGCTCAGAATATCTCCATCAAGTGTTAAACTACATATTTCATTC 7900
AAATTTATATAGAAAACGATAATTAAGGTGAAAACTTTTATAAAGATATC 7950
GTGTGGTTGTGTGAGTGAGGTGACAAAATAAGTTGTGTGATTATTCAAAA 8000
AGTTTTAATAACGAAAATCCACATGCTTGAATTAATTGAAGCATTAATGT 8050
TGTAACGAAAAATATTACATTTATTGAGTTACTGTGATGTTTTAACTGAT 8100
ATATAAAATAATATTGGTATTTCTCTTCATCTGCGACATAATATGTTTTT 8150
TCATCTTTTTTCAATATACAAAATAGAATTATTATTTTGTTGCATCTTTT 8200
TAAGTACAAATTATTCATATGTATATAGTACAAAATAAAATATTTACTGT 8250
GGTAAAGTAAATGGAATAAGAGGTCATATTTGAAATAACAATATACTATA 8300
CTATGTTAAAGTATTTTTTATAGTTAAAATTTCTCTAGAGTACTTGATTC 8350
TACATACAAATACTAATTTCGTAAAAAAATTAATATTGAATTTCTTCATT 8400
GTTTCTTTATTATTAAATTAGTTTATAATAACTAAACTAAGGTAATAAGA 8450
CCTTAGTTTAGTTAATGTGTGTCTCTGTGATTTCGTTCATAGTCTAAGGG 8500
TGTACTTGTGCCTTATCCCAAAAATGAAGGAATATCAAAAGATATATTAA 8550
AATTAAATTAAATATTTGGAGGTTATGAATATAAAAAGTATCAGAGTTCT 8600
ACATATAAAGAGTAACAATTGAAATAATTAATTAAATATGAGATATGAAG 8650

GCGGACATTTAAAGAAAATAATAAATAAATAAATTAAAGGGTATAAATTT 8700
CATAATACATAATACCAATAAGCCGTAGAATATCTCCGTCATAATGCATA 8750
AACTAATAAATCACAAATGTATAACTCACATACAAATATTTTTTGATAAA 8800
GAATTTGAATGTTGTAATAGAATGGAGAATAACTTGTGTCTTATTCCATT 8850
ATGTAAGACGTATAAATACAAATACAATGAGCTCTAATTAATTAAGGAAA 8900
CTAAATAAGGAAGGAATCAAAAAATATTATGTCATATCCCTACATATCTG 8950
CTAGAGATTCTATCATATCCTTACATATCTGTTAAGCTATGTCTACACCT 9000
AAAGGTGTCTACAATCATTTTGTAACACTCCCCCTCAAGTTAGAGCATAG 9050
ATATTATTCATTCCCAACTTGTTACAAAGATAATCAACTCGAGTTCCATT 9100
CAACGCTTTTGTGAACAAATCAACTAGTTGCTCTCCTGTCTTCACTTAGC 9150
TAGTGGATATCAGGTTTTCATGAATCTTCTCACGAATAAAATGACAGTCA 9200
ACCTCAATATGTTTAGTTCTTTCATGAGACACCGGATTCAAGGCAATATG 9250
GAGCGCAACTTGATTATCATACTAGAGTTTTGATGGTATATGATGCTTCA 9300
ACCCTATTTCTGTTAAAAGATAATGTATCCACATGATCTCACCCATAGAC 9350
TGTAACATAACTCTGTACTTTGATTCTGCACTAGATCAAGATACAACATT 9400
TTGCTTTTTACTCCTCCATGATACCAGGTTTCATCCAACAAAGACACAAT 9450
AACTTGTAGTAGATCTTCTATCAATTTTCGATCCAGCCCAATCGACATCT 9500
GCAAAACACTCAATATGAGTATGGTCGTGATTTTGATACTATATTCCAAG 9550
ACTAGGAGTTTTCTTCAAGTAACATAGAATATGTTCCAAAGCTGCCCAGT 9600
GTTTGACGTAGGTGCAAACATGAACTAGCTAACAACACTTACTGCAAAAG 9650
CAATATCAAGATGAGTCACAATAAGGTAGTTTAACTTTCCAACTAACCTT 9700
TTGTATCTCTATGGATCATTAAAAGGATCGTCGTCATCTTTCATAAGATG 9750
CATATTGGGAACCATTGGAGAACTTCAGGGTTTGGCTGCCATCTTTCAAT 9800
TTTCTGCAAGTAGATCGAGAGAATATATTCTCTAAGACAAAAGAATTCCC 9850
TTTTTGTTTCTATTTACTTCTACTCCCAAAATGTATTTCAATTGACCCAA 9900
GTCCTTCGTATGAAACCAAGTATGCAGGAAAGACTTGAGGGAAGAGATC 9949

A

B

LZ

MEKRKDNEEANNSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIE
SLKLKLTFICTYVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDV
GCKYVLTSLAGNMDDCISLYHRSKSDATMMDEQLGFLLLNLSHLSKHRA
EKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCIKHEMVENVLSLFQLMAE
RVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIVPTELEV
MHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPN
TSGARNIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTL
VRDLEEKLRIKESTDETNCATLKFLENIELLKEDLKHVYLKVPDSSQYC
FPMSDGPLFMHLLQRHLDDLLDSNAYSIALIKEQIGLVKEDLEFIRSFF
ANIEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLLHLIFSLPITRKK
MMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEET

NBS

NLILRKLTSGPADLDVISII*gmpglgkttla*YKVYNDKSVSSHFDLRAW
CTVDQVYDEKKLLDKIFNQVSDSNSKLSENIDVADKLRKQLFG*kryliv*
*lddvw*DTNTWDELTRPFPDGMKG*sriilttr*EKKVALHGKLYTDPLNLR
LLRSEESWELLEKRAFGNESCPDELLDVGKEIAENCK*glplvvdliag*I
IAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH*lkpcll*
*yfas*APKDWVTTIHELKLIWGFEGFVEKTDMKSLEEVVKIYLDDLISSS
LVICFNEIGDYPTCQlhdlvhdFCLIKARKEKLCDRISSSAPSDLLPRQ
ISIDYDD

LRR

DEEHFGLNFVLFGSNKK	1
RHSGKHLYSLTINGDE.LDDHLSDTFH	2
LRHLRLLRTLHLESSFIMVKDSLLNE	3
ICMLNHLRYLSIGTEVKSLPLSF	4
SNBLWNLEILFVDNKESTLIL	5
LPRIWDLVKLQVLFTTACS	6
FFDMDADESILIAEDTK	7
LENLTALGELVLSYWKDT	8
EDIFKRLPNLQVLHFK.LKESWDYSTEQYWFPK	9
LDFLTELEKLTVDFERSNTNDSGSSAAINRPWD	10
FHFPSSLKRLQLHEFP.LTSDSLST	11
IARLLNLEELYLYRTI.IHGEEWNMGE	12
EDTFENLKCLMLSQVI.LSKWEVG	13
EESFPTLEKLELSDCHNLEEIPSS	14
FGDIYSLKIIELVRSPQLENSALK	15

IKEYAEDMRGGDELQILGQKDIPLFK

FIGURE 14

```
Mi1.1                    VL    S  I D  V   ---   N   L K QV KI    MA
57
Mi1.2           I        VL    S  I    I   ---   N   L K QV KL    MA
57
Rpi-blb2    MEKRKDNEEANNSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIESLKLKLTFICT
60

Mi1.1            C  F Q                  L    --------- F   TS
109
Mi1.2            Y  F Q        N         SL   --------     TS
109
Rpi-blb2    YVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR
120

Mi1.1         Y    I       D       Y     H   I              I              G
169
Mi1.2         Y    I       D       Y     H   I                             L G
169
Rpi-blb2    S-KSDATMMDEQLGFLLLNLSHLSKHRAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI
179

Mi1.1               P       D   H   D  T    R        E    R SR
229
Mi1.2               P           H       T    R        EH   R SR  Q T
229 Rpi-blb2
      KHEMVENVLSLFQLMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV 239

Mi1.1         V    I     TN        A V L   Q                P      V      S
289
Mi1.2                    TN        A V                      I Q      L    P S L
289
Rpi-blb2    PTELEVMHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPNTSGAR
299

Mi1.1               L       -               D  GV                  EP N   GNNQ
348
Mi1.2               L       -                H GT                     N   GNNQ
348
Rpi-blb2    NIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTLVRDLEEKLRIKESTDE
359

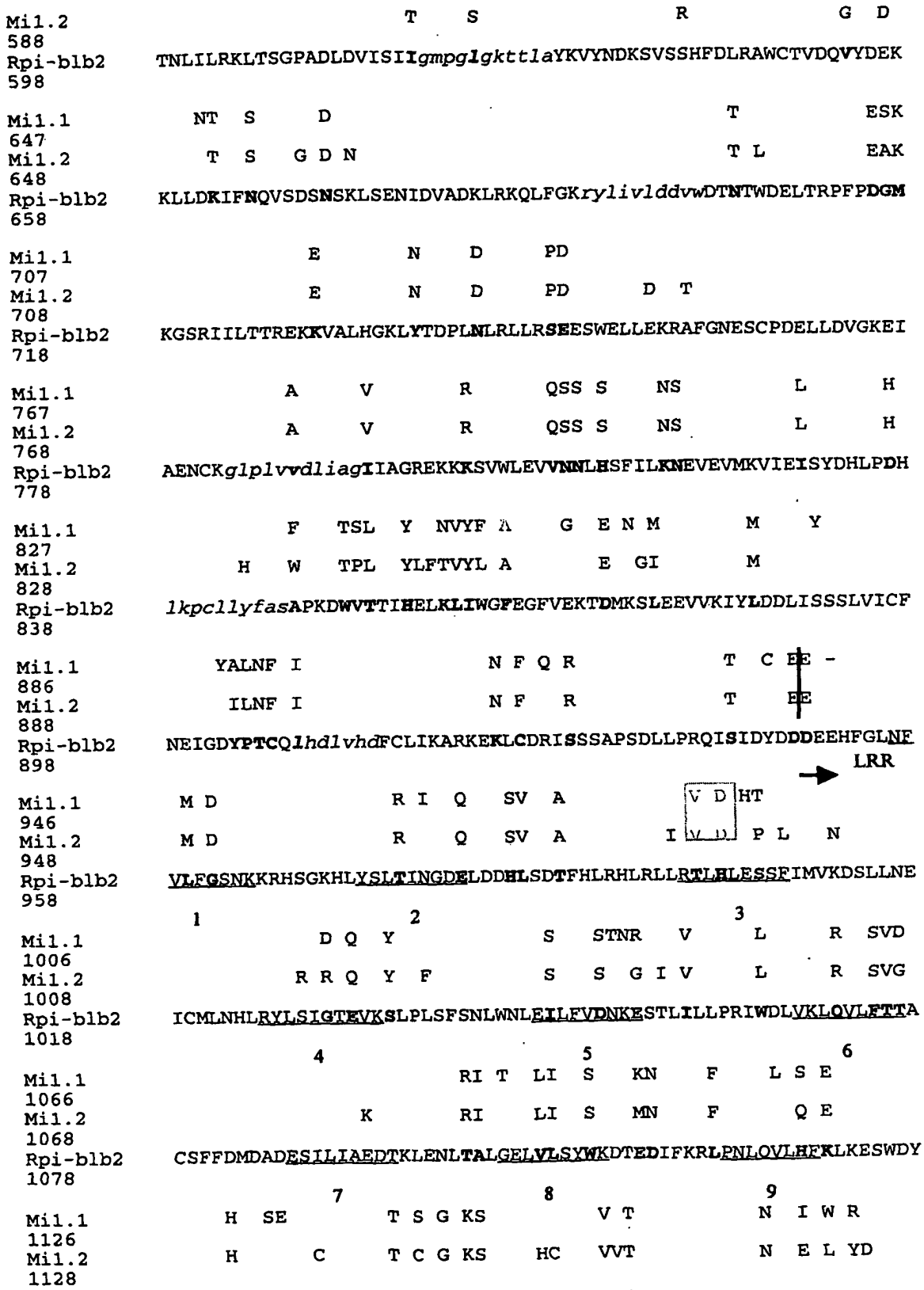
Mi1.1            DL         K         AL    C                HI   N
408
Mi1.2            DL         K         A N   C                HM   N
408
Rpi-blb2    TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDDLLDSNAYS
419

Mi1.1              E E   Q  K       VD-A          A
467
Mi1.2         S    E E   SQE        GDAA        I A
468
Rpi-blb2    IALIKEQIGLVKEDLEFIRSFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL
478         ----------------

Mi1.1               I  IK     I A D   P D                R         T   E
527
Mi1.2               I  IK     I A D   P D                R         I   E
528
Rpi-blb2    HLIFSLPITRKKMMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEE
538

Mi1.1                  S        T     S                  R           GC
587
```

FIGURE 15


Mi1.2
588
Rpi-blb2
598
Mi1.1
647
Mi1.2
648
Rpi-blb2
658
Mi1.1
707
Mi1.2
708
Rpi-blb2
718
Mi1.1
767
Mi1.2
768
Rpi-blb2
778
Mi1.1
827
Mi1.2
828
Rpi-blb2
838
Mi1.1
886
Mi1.2
888
Rpi-blb2
898
LRR
Mi1.1
946
Mi1.2
948
Rpi-blb2
958
1
2
3
Mi1.1
1006
Mi1.2
1008
Rpi-blb2
1018
4
5
6
Mi1.1
1066
Mi1.2
1068
Rpi-blb2
1078
7
8
9
Mi1.1
1126
Mi1.2
1128

```
Rpi-blb2    STEQYWFPKLDFLTELEKLTVDFERSNTNDSGSSAAINRPWDFHFPSSLKRLQLHEFPLT
1138
                                  10                                  11
Mi1.1                P      S  H                        F NFN  SI
1186
Mi1.2                P   N  S  D   Q                    F N RLLT
1188
Rpi-blb2    SDSLSTIARLLNLEELYLYRTIIHGEEWNMGEEDTFENLKCLMLSQVILSKWEVGEESFP
1198
                          12                                  13
Mi1.1       N    K RG  K     P          S KI K     D
1246
Mi1.2       N    K QE GK     P          F KI K     D       K          ND
1248
Rpi-blb2    TLEKLELSDCHNLEEIPSSFGDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL
1258
                 14                            15
Mi1.1          N       1255
Mi1.2          N       1257
Rpi-blb2    GQKDIPLFK 1267
```

Figure 16: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-blb2 nucleic acids

```
CLUSTAL W (1.82) Multiple Sequence Alignments


Sequence format is Pearson
Sequence 1: Mi1.1           3768 bp
Sequence 2: Mi1.2           3774 bp
Sequence 3: Rpi-blb2        3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:  95
Sequences (1:3) Aligned. Score:  89
Sequences (2:3) Aligned. Score:  89
Guide tree        file created:   [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:   2      Score:68908
Group 2: Sequences:   3      Score:65855
Alignment Score 66872
CLUSTAL-Alignment file created  [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14435620.aln]


CLUSTAL W (1.82) multiple sequence alignment
```

Figure 17: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-blb2 proteins

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mi1.1 1255 aa
Sequence 2: Mi1.2 1257 aa
Sequence 3: Rpi-blb2 1267 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 91
Sequences (1:3) Aligned. Score: 82
Sequences (2:3) Aligned. Score: 81
Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-14322840.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:25939
Group 2: Sequences: 3 Score:24668
Alignment Score 19405
CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-14322840.aln]

CLUSTAL W (1.82) multiple sequence alignment

```
Mi1.1           MEKRKDNEEANNSLVLFSALSKDIADVLVFLE---NEENQKALDKDQVEKIKLKMAFICT 57
```

```
Mi1.2          MEKRKDIEEANNSLVLFSALSKDIANVLIFLE---NEENQKALDKDQVEKLKLKMAFICT 57
Rpi-blb2       MEKRKDNEEANNSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIESLKLKLTFICT 60
               ****** *******  **** ** *:** ***   ***:***:* * :*.:***::****

Mi1.1          YVQLSCSDFEQFEDIMTRKRQEVENLLQPLLDDD--------VFTSLTSNMDDCISLYHR 109
Mi1.2          YVQLSYSDFEQFEDIMTRNRQEVENLLQSLLDDD--------VLTSLTSNMDDCISLYHR 109
Rpi-blb2       YVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR 120
               ***** **:*:*******:*********.:****        *:***:.**********

Mi1.1          SYKSDAIMMDEQLDFLLLNLYHLSKHHAEKIFPGVTQYEVLQNICGNIRDFHGLIVNGCI 169
Mi1.2          SYKSDAIMMDEQLDFLLLNLYHLSKHHAEKIFPGVTQYEVLQNVCGNIRDFHGLILNGCI 169
Rpi-blb2       S-KSDATMMDEQLGFLLLNLSHLSKHRAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI 179
               * **** ******.****** *****:***:***********:**********:* **

Mi1.1          KHEMVENVLPLFQLMADRVGHFLWDDQTDEDSRLSELDEDEQNDRDSRLFKLAHLLLKIV 229
Mi1.2          KHEMVENVLPLFQLMAERVGHFLWEDQTDEDSRLSELDEDEHNDRDSRLFQLTHLLLKIV 229
Rpi-blb2       KHEMVENVLSLFQLMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV 239
               *********.******:***:***:**:****:*******::**:*.:**:*:*******

Mi1.1          PVELEVIHICYTNLKASTSAEVGLFIKQLLETSPDILREYLIPLQEHMVTVITPSTSGAR 289
Mi1.2          PTELEVMHICYTNLKASTSAEVGRFIKKLLETSPDILREYIIQLQEHMLTVIPPSTLGAR 289
Rpi-blb2       PTELEVMHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPNTSGAR 299
               *.****:****..******:*:* ***:************:* *****:***.*.* ***

Mi1.1          NIHVMMEFLLLILSDMP-KDFIHHDKLFDLLDRVGVLTREVSTLVRDLEEEPRNKEGNNQ 348
Mi1.2          NIHVMMEFLLLILSDMP-KDFIHHDKLFDLLAHVGTLTREVSTLVRDLEEKLRNKEGNNQ 348
Rpi-blb2       NIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTLVRDLEEKLRIKESTDE 359
               **********:****** ************* :* .**************: * **..::

Mi1.1          TNCATLDLLENIELLKKDLKHVYLKALDSSQCCFPMSDGPLFMHLLHIHLNDLLDSNAYS 408
Mi1.2          TNCATLDLLENIELLKKDLKHVYLKAPNSSQCCFPMSDGPLFMHLLHMHLNDLLDSNAYS 408
```

```
Rpi-blb2        TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDDLLDSNAYS 419
                ******.:********:********. :*** **************: **:*********

Mi1.1           IALIKEEIELVKQDLKFIRSFFVD-AEQGLYKDLWARVLDVAYEAKDVIDSIIVRDNGLL 467
Mi1.2           ISLIKEEIELVSQELEFIRSFFGDAAEQGLYKDIWARVLDVAYEAKDVIDSIIVRDNGLL 468
Rpi-blb2        IALIKEQIGLVKEDLEFIRSFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL 478
                *:****:* **.::*:****** :  *******:* **********************

Mi1.1           HLIFSLPITIKKIKLIKEEISALDENIPKDRGLIVVNSPKKPVERKSLTTDKITVGFEEE 527
Mi1.2           HLIFSLPITIKKIKLIKEEISALDENIPKDRGLIVVNSPKKPVERKSLTTDKIIVGFEEE 528
Rpi-blb2        HLIFSLPITRKKMMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEE 538
                ********* **: *****:* *.***.*:************** ******** *** **

Mi1.1           TNLILRKLTSGSADLDVISITGMPGSGKTTLAYKVYNDKSVSSRFDLRAWCTVDQGCDEK 587
Mi1.2           TNLILRKLTSGPADLDVISITGMPGSGKTTLAYKVYNDKSVSRHFDLRAWCTVDQGYDDK 588
Rpi-blb2        TNLILRKLTSGPADLDVISIIGMPGLGKTTLAYKVYNDKSVSSHFDLRAWCTVDQVYDEK 598
                **********.******** **** ********************** :***********  *:*

Mi1.1           KLLNTIFSQVSDSDSKLSENIDVADKLRKQLFGKRYLIVLDDVWDTTTWDELTRPFPESK 647
Mi1.2           KLLDTIFSQVSGSDSNLSENIDVADKLRKQLFGKRYLIVLDDVWDTTTLDELTRPFPEAK 648
Rpi-blb2        KLLDKIFNQVSDSNSKLSENIDVADKLRKQLFGKRYLIVLDDVWDTNTWDELTRPFPDGM 658
                ***:.**.***.*:*:*********************************.* ********:.

Mi1.1           KGSRIILTTREKEVALHGKLNTDPLDLRLLRPDESWELLEKRAFGNESCPDELLDVGKEI 707
Mi1.2           KGSRIILTTREKEVALHGKLNTDPLDLRLLRPDESWELLDKRTFGNESCPDELLDVGKEI 708
Rpi-blb2        KGSRIILTTREKKVALHGKLYTDPLNLRLLRSEESWELLEKRAFGNESCPDELLDVGKEI 718
                ************:******* ****:*****.:******:**:*****************

Mi1.1           AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFILNSEVEVMKVIELSYDHLPHH 767
Mi1.2           AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFILNSEVEVMKVIELSYDHLPHH 768
Rpi-blb2        AENCKGLPLVVDLIAGIIAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH 778
```

```
                  **********.*****:*******:****** ..* ****:.*********:******.*

Mi1.1             LKPCLLYFASFPKDTSLTIYELNVYFGAEGFVGKTEMNSMEEVVKIYMDDLIYSSLVICF 827
Mi1.2             LKPCLLHFASWPKDTPLTIYLFTVYLGAEGFVEKTEMKGIEEVVKIYMDDLISSSLVICF 828
Rpi-blb2          LKPCLLYFASAPKDWVTTIHELKLIWGFEGFVEKTDMKSLEEVVKIYLDDLISSSLVICF 838
                  ******:*** ***   **: :.:  * **** **:*:.:*******:**** *******

Mi1.1             NEIGYALNFQIHDLVHDFCLIKARKENLFDQIRSSAPSDLLPRQITIDCDEEE-HFGLNF 886
Mi1.2             NEIGDILNFQIHDLVHDFCLIKARKENLFDRIRSSAPSDLLPRQITIDYDEEEEHFGLNF 888
Rpi-blb2          NEIGDYPTCQLHDLVHDFCLIKARKEKLCDRISSSAPSDLLPRQISIDYDDDEEHFGLNF 898
                  ****   . *:****************:* *:* ************:** *::* ******

Mi1.1             VMFDSNKKRHSGKHLYSLRIIGDQLDDSVSDAFHLRHLRLLRVLDLHTSFIMVKDSLLNE 946
Mi1.2             VMFDSNKKRHSGKHLYSLRINGDQLDDSVSDAFHLRHLRLIRVLDLEPSLIMVNDSLLNE 948
Rpi-blb2          VLFGSNKKRHSGKHLYSLTINGDELDDHLSDTFHLRHLRLLRTLHLESSFIMVKDSLLNE 958
                  *:*.************** * **:*** :**:********:*.*.*..*:***:******

Mi1.1             ICMLNHLRYLSIDTQVKYLPLSFSNLWNLESLFVSTNRSILVLLPRILDLVKLRVLSVDA 1006
Mi1.2             ICMLNHLRYLRIRTQVKYLPFSFSNLWNLESLFVSNKGSILVLLPRILDLVKLRVLSVGA 1008
Rpi-blb2          ICMLNHLRYLSIGTEVKSLPLSFSNLWNLEILFVDNKESTLILLPRIWDLVKLQVLFTTA 1018
                  ********** * *:** **:********* ***..: * *:***** *****:** . *

Mi1.1             CSFFDMDADESILIAEDTKLENLRILTELLISYSKDTKNIFKRFPNLQLLSFELKESWDY 1066
Mi1.2             CSFFDMDADESILIAKDTKLENLRILGELLISYSKDTMNIFKRFPNLQVLQFELKESWDY 1068
Rpi-blb2          CSFFDMDADESILIAEDTKLENLTALGELVLSYWKDTEDIFKRLPNLQVLHFKLKESWDY 1078
                  ***************:*******  * **::** *** :****:****:* *:*******

Mi1.1             STEQHWFSELDFLTELETLSVGFKSSNTNDSGSSVATNRPWDFHFPSNLKILWLREFPLT 1126
Mi1.2             STEQHWFPKLDCLTELETLCVGFKSSNTNHCGSSVVTNRPWDFHFPSNLKELLLYDFPLT 1128
Rpi-blb2          STEQYWFPKLDFLTELEKLTVDFERSNTNDSGSSAAINRPWDFHFPSSLKRLQLHEFPLT 1138
                  ****:**.:** *****.* *.*: ****..***.. **********.** * * :****
```

```
Mi1.1       SDSLSTIARLPNLEELSLYHTIIHGEEWNMGEEDTFENLKFLNFNQVSISKWEVGEESFP 1186
Mi1.2       SDSLSTIARLPNLENLSLYDTIIQGEEWNMGEEDTFENLKFLNLRLLTLSKWEVGEESFP 1188
Rpi-blb2    SDSLSTIARLLNLEELYLYRTIIHGEEWNMGEEDTFENLKCLMLSQVILSKWEVGEESFP 1198
            ********** ***:* ** ***:**************** * :  : :***********

Mi1.1       NLEKLKLRGCHKLEEIPPSFGDIYSLKSIKIVKSPQLEDSALKIKEYAEDMRGGDELQIL 1246
Mi1.2       NLEKLKLQECGKLEEIPPSFGDIYSLKFIKIVKSPQLEDSALKIKKYAEDMRGGNDLQIL 1248
Rpi-blb2    TLEKLELSDCHNLEEIPSSFGDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL 1258
            .****:*  * :*****.********* *::*:*****:******:********::****

Mi1.1       GQKNIPLFK 1255
Mi1.2       GQKNIPLFK 1257
Rpi-blb2    GQKDIPLFK 1267
            ***:*****
```

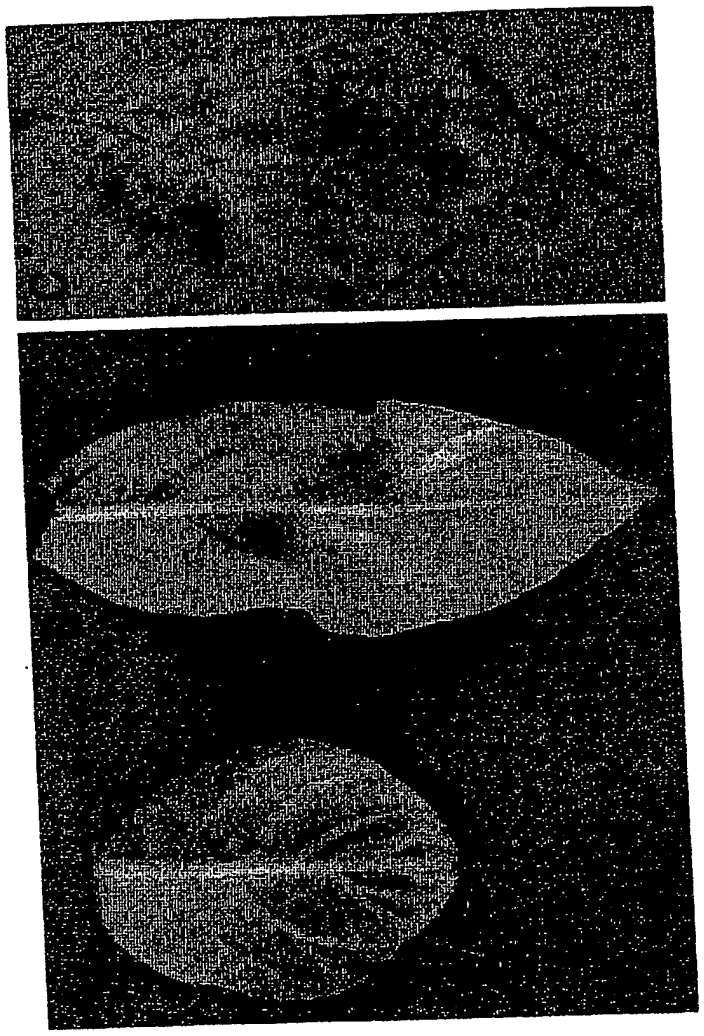


Figure 18